## UNITED STATES PATENT AND TRADEMARK OFFICE CERTIFICATE OF CORRECTION

PATENT NO. : 7,276,589 B2 Page 1 of 29

APPLICATION NO.: 10/724274
DATED: October 2, 2007
INVENTOR(S): Ramakrishnan et al.

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

## In the Specification:

Please replace the Sequence Listing beginning at column 35, line 40 with the substitute Sequence Listing submitted.

## In the Claims:

In Claim 9, column 72, line 49:

Please replace "carder" with --carrier--.

Signed and Sealed this

Twenty-eighth Day of October, 2008

JON W. DUDAS
Director of the United States Patent and Trademark Office

## SEQUENCE LISTING

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<110> Protein Design Labs, Inc.
Ramakrishnan, Vanitha
Powers, David
Johnson, Dale E
Jeffry, Ursula
Bhaskar, Vinay
```

- <120> Chimeric and Humanized Antibodies to alpha5betal Integrin That Modulate Angiogenesis
- <130> 05882.0178.NPUS01
- <140> 10/724,274
- <141> 2003-11-26
- <150> 60/429,743 <151> 2002-11-26
- <150> 60/508,149
- <151> 2003-09-30
- <160> 47
- <170> PatentIn version 3.2
- <210> 1
- <211> 124
- <212> PRT <213> mus musculus
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Ser Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu Thr Asp Tyr 20 25 30

Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu 35 40 45

Val Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser Ala Leu Lys 50 60

Ser Arg Met Thr Ile Arg Lys Asp Asn Ser Lys Ser Gln Val Phe Leu 70 75 80

Ile Met Asn Ser Leu Gln Thr Asp Asp Ser Ala Met Tyr Tyr Cys Ala 85 90 95

Arg His Gly Thr Tyr Tyr Gly Met Thr Thr Thr Gly Asp Ala Leu Asp 100 105

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Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu 35 40 45
Val Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser Ala Leu Lys 50 60
Ser Arg Met Thr Ile Ser Lys Asp Asn Ser Lys Ser Thr Val Tyr Leu 65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95
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Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu 35 40 45
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Ser Arg Met Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Tyr Leu 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

Arg His Gly Thr Tyr Tyr Gly Met Thr Thr Gly Asp Ala Leu Asp 100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 115 120

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Ser Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser Ala Leu Lys 50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

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Val Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser Ala Leu Lys 50 55
Ser Arg Met Thr Ile Ser Lys Asp Asn Ser Lys Ser Thr Val Tyr Leu 65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
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Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 115 120
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Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu 35 40 45
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Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Ser Ala Pro Asn Leu Trp
35 40 45

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu 65 70 75 80

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Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

Asp Arg Val Thr Met Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Asn 20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp 35 40 45

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser 50 60

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Met Gln 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Leu Arg Ser Pro 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

<sup>&</sup>lt;210> 9

<sup>&</sup>lt;211> 109

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Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser 50 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln 65 70 75 80

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Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser

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Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln 65 70 80

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PRT

Artificial Sequence

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Asp Arg Val Thr Met Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Asn 20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp
35 40 45

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln 65 70 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Leu Arg Ser Pro 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

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gctctcaaat ccagaatgac catca	ggaag gacaactcca agagccaagt tttcttaata 300
atgaacagtc tccaaactga tgact	cagcc atgtactact gtgccagaca tggaacttac 360
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Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu 35 40 45
Thr Asp Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu 50 60
Glu Trp Leu Val Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser 65 70 75 80
Ala Leu Lys Ser Arg Met Thr Ile Arg Lys Asp Asn Ser Lys Ser Gln
Val Phe Leu Ile Met Asn Ser Leu Gln Thr Asp Asp Ser Ala Met Tyr 100 105
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cagaagccag gatccgcccc caatctctgg atttatagca catccaacct ggcttctgga
                                                                          300
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                                                                          360
atggaggctg aagatgctgc cacttattac tgccaccagt atcttcgttc cccaccgacg
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20 25 30
Met Ser Ala Ser Leu Gly Glu Arg Val Thr Met Thr Cys Thr Ala Ser 35 40 45
Ser Ser Val Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly 50 60
Ser Ala Pro Asn Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly 65 70 75 80
Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
85 90 95
Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His
100 105 110
Gln Tyr Leu Arg Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys
130
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300

360

420 459

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20 25 30
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Thr Asp Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu 50 60
Glu Trp Leu Val Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser 65 70 75 80
Ala Leu Lys Ser Arg Met Thr Ile Arg Lys Asp Asn Ser Lys Ser Gln
85 90 95
Val Phe Leu Ile Met Asn Ser Leu Gln Thr Asp Asp Ser Ala Met Tyr 100 105 110
Tyr Cys Ala Arg His Gly Thr Tyr Tyr Gly Met Thr Thr Thr Gly Asp 115
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Met Ser Ala Ser Leu Gly Glu Arg Val Thr Met Thr Cys Thr Ala Ser 35 40 45

Ser Ser Val Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly 50 60

Ser Ala Pro Asn Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly 65 75 80

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu 85 90 95

Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His 100 105 110

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                                                                     180
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                                                                     300
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                                                                     960
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Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu 35 40 45

Val Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser Ala Leu Lys 50 60

Ser Arg Met Thr Ile Arg Lys Asp Asn Ser Lys Ser Gln Val Phe Leu 65 70 75 80

Ile Met Asn Ser Leu Gln Thr Asp Asp Ser Ala Met Tyr Tyr Cys Ala 85 90 95

Arg His Gly Thr Tyr Tyr Gly Met Thr Thr Thr Gly Asp Ala Leu Asp 100 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
115
125

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Artificial Sequence

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265 270 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr 290 295 300 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 315 310 315 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile 325 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 340 345 350 Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser 355 360 365 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 370 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 405 415

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met 420 430

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Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser 50 60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu 65 70 75 80

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Tyr Leu Arg Ser Pro

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala 100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu

135

140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser 145 Glm Glu Ser Val Thr Glu Glm Asp Ser Lys Asp Ser Thr Tyr Ser Leu 165 170 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val 180 185 190 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys 195 200 205 Ser Phe Asn Arg Gly Glu Cys <210> 27 696 <212> DNA <213> Artificial Sequence <220> <223> chimeric antibody <400> 27 caggigage igaaggagic aggaceigge eiggiggege ceteacagag ceigtecate 60 acatgcacca tctcagggtt ctcattaacc gactatggtg ttcactgggt tcgccagcct 120 ccaggaaagg gtctggagtg gctggtagtg atttggagtg atggaagctc aacctataat 180 tcagctctca aatccagaat gaccatcagg aaggacaact ccaagagcca agttttctta 240 ataatgaaca gtctccaaac tgatgactca gccatgtact actgtgccag acatggaact 300 tactacggaa tgactacgac gggggatgct ttggactact ggggtcaagg aacctcagtc 360 accytctcct caycttccac caaggyccca tecytcttcc cectygcycc ctyctccagy 420 agcacctccg agagcacagc cgccctgggc tgcctggtca aggactactt ccccgaaccg 480 gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540 ctacagteet caggacteta eteceteage agegtggtga cegtgeete cageagettg 600 ggcacgaaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag 660 agagttgagt ccaaatatgg tcccccatgc ccatca 696 28 232 Artificial Sequence

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115 120 125 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu 130 135 140 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 145 150 155 160 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 165 170 175 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 180 185 190 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn 200 205 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser 210 220 Lys Tyr Gly Pro Pro Cys Pro Ser 225

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                                                                     180
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Val Val Ile Trp Ser Asp Gly Ser Ser Thr Tyr Asn Ser Ala Leu Lys 50 60

Ser Arg Met Thr Ile Ser Lys Asp Asn Ala Lys Asn Thr Val Tyr Leu 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

Arg His Gly Thr Tyr Tyr Gly Met Thr Thr Thr Gly Asp Ala Leu Asp 100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu 130 135 140 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 145 150 155 160 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 180 185 190 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn 195 200 205 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser 210 215 220 Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly 225 235 240 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser Gln 265 270 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val. 275 280 285 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr 290 295 300 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 305 310 315 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile 325 330 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser 355 360 365 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 370 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 405 415

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 435 440 445

Leu Gly Lys 450

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Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser 50 60

Gly Ser Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Ser Ser Leu Glu 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Tyr Leu Arg Ser Pro 85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala 100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser 115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu

140

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Gln Glu Ser val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
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mus musculus

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Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile 20 25 30

Met Ser Ala Ser Leu Gly Glu Arg Val Thr Met Thr Cys Thr Ala Ser

Ser Ser Val Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly 50 60

Ser Ala Pro Asn Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly 65 70 75 80

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu 85 90 95

Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His 100 105 110

Gln Tyr Leu Arg Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu 125

Ile Lys